

OIPE

## RAW SEQUENCE LISTING

DATE: 05/03/2000

PATENT APPLICATION: US/09/548,717

TIME: 16:30:47

Input Set : A:\200017.app

Output Set: N:\CRF3\050300\I548717.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Toyo Boseki Kabushiki Kaisha  
 5 <120> TITLE OF INVENTION: METHOD OF EXTRACTING NUCLEIC ACIDS USING PARTICULATE  
 6 CARRIER  
 8 <130> FILE REFERENCE: 200017  
 10 <140> CURRENT APPLICATION NUMBER: US/09/548,717  
 11 <141> CURRENT FILING DATE: 2000-04-13  
 13 <160> NUMBER OF SEQ ID NOS: 4  
 15 <170> SOFTWARE: PatentIn Ver. 2.1  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 24  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: Artificial Sequence  
 22 <220> FEATURE:  
 23 <223> OTHER INFORMATION: Description of Artificial Sequence:comprising a  
 24 sequence complementary to the nucleotides 102  
 25 through 125 of the nucleotide sequence of V.  
 26 parahaemolyticus TDH (Thermostable Direct  
 27 Haemolysin) gene.  
 29 <400> SEQUENCE: 1  
 30 ccccggttct gatgagatat tggt 24  
 33 <210> SEQ ID NO: 2  
 34 <211> LENGTH: 51  
 35 <212> TYPE: DNA  
 36 <213> ORGANISM: Artificial Sequence  
 38 <220> FEATURE:  
 39 <223> OTHER INFORMATION: Description of Artificial Sequence:comprising a  
 40 sequence complementary to the nucleotides 495-518  
 41 of the nucleotide seq. of V. parahaemolyticus TDH  
 42 gene, and a promoter sequence for T7-RNA  
 43 polymerase.  
 45 <400> SEQUENCE: 2  
 46 aattctaata cgactcacta tagggagacc aatatattac cactaccact a 51  
 49 <210> SEQ ID NO: 3  
 50 <211> LENGTH: 26  
 51 <212> TYPE: DNA  
 52 <213> ORGANISM: Artificial Sequence  
 54 <220> FEATURE:  
 55 <223> OTHER INFORMATION: Description of Artificial Sequence:comprising a  
 56 sequence complementary to the nucleotides 339  
 57 through 364 of the nucleotide sequence of V.  
 58 parahaemolyticus TDH (Thermostable Direct  
 59 Haemolysin) gene.  
 61 <400> SEQUENCE: 3  
 62 cggtcattct gctgtgttcg taaaat 26  
 65 <210> SEQ ID NO: 4  
 66 <211> LENGTH: 24  
 67 <212> TYPE: DNA

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/548,717

DATE: 05/03/2000  
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Input Set : A:\200017.app  
Output Set: N:\CRF3\050300\I548717.raw

68 <213> ORGANISM: Artificial Sequence  
70 <220> FEATURE:  
71 <223> OTHER INFORMATION: Description of Artificial Sequence:comprising a  
72 sequence complementary to the nucleotides 254  
73 through 277 of the nucleotide sequence of V.  
74 parahaemolyticus TDH (Thermostable Direct  
w-OK 75 Haemolysin) gene.  
77 <400> SEQUENCE: 4  
W--> 78 cagg tactaa ~~at~~gggttgaca tcct

24

*see item 10 on Error Summary Sheet*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/548,717

DATE: 05/03/2000

TIME: 16:30:48

Input Set : A:\200017.app

Output Set: N:\CRF3\050300\I548717.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number  
 L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:27 M:259 W: Field exceeds allowed number of lines, <223> Other Information:  
 L:43 M:259 W: Field exceeds allowed number of lines, <223> Other Information:  
 L:59 M:259 W: Field exceeds allowed number of lines, <223> Other Information:  
 L:75 M:259 W: Field exceeds allowed number of lines, <223> Other Information:  
 L:78 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4  
 L:78 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4  
 L:78 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/548,917

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      **(2) INFORMATION FOR SEQ ID NO:X:**  
                                 (i) **SEQUENCE CHARACTERISTICS:**(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
                                 (xi) **SEQUENCE DESCRIPTION:SEQ ID NO:X:**  
                                 **This sequence is intentionally skipped**  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      **<210> sequence id number**  
                                 **<400> sequence id number**  
                                 **000**
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism      Sequence(s)        are missing this mandatory field or its response.  
(NEW RULES)
- 12        Use of <220>Feature      Sequence(s)        are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
                                 **Please explain source of genetic material in <220> to <223> section.**  
                                 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      **Please do not use "Copy to Disk" function of PatentIn version 2.0.** This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.